

cDNA Sequence of human IBR

Two alternative 5' ends:

1 TTGAGGAACAGGCAGACTCCACAGCTCCGCCAGGAGAA
2 AAGGAAGGAGGGAGAAGGGAAGGAGTGAAGGAAGGAGTGAAA

Common Sequence:

AGGGAGTCTACACCCTGTGGAGCTCAAGATGGTCCTGAGTGGGGCGCTGTGCTTCCGAA 60
TGAAGGACTCGGCATTGAAGGTGTTATCTGCATAATAACCAGCTCTAGCTGGAGGGC 120
TGCATGCAGGGAAAGGTCATTAAGGTGAAGAGATCAGCGTGGTCCCCAATCGGTGGCTGG 180
ATGCCAGCCTGTCCCCGTCATCCTGGGTGTCCAGGGTCCAAGGCCAGTGCCTGTCA 240
TG
GGGTGGGGCAGGAGCCACTCTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTG 300
GTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGCGGGACATGGGCTCACCTCCAGCT 360
TCGAGTCGGCTGCCTACCGGGCTGGTCTGTGCACGGTGCCTGAAGCCGATCAGCCTG 420
TCAGACTCACCCAGCTTCCCAGAATGGTGGCTGGAATGCCCATCACAGACTTCTACT 480
TCCAGCAGTGTGACTAGGGCAACGTGCCCCCCCAGAACTCCCTGGCAGAGCCAGCTCGG 540
GTGAGGGGTGAGTGGGAGGAGACCCATGGCGGACAATCACTCTTGCTCTCAGGACCCC 600
CAGGTCTGACTTAGGGCACCTGACCACTTGTCTGGTCCCAGTTGCATAAATT 660
CTGAGATTGGAGCTCAGTCCAGGGCTCCCCACTGGATGGTCTACTGCTGTGGAAC 720
CTTGTAAAAACCATGTGGGTAAACTGGGAATAACATGAAAAGATTCTGTGGGGGTGGG 780
GTGGGGAGTGCTGGAATCATTCTGCTTAATGGTAAGTGACAAGTGTACCCCTGAGCC 840
CCGCAGGCCAACCCATCCCCAGTTGAGCCTATAGGGTCAGTAGCTCCACATGAAGTC 900
CTCTCACTCACCCTGTGCAGGAGAGGGAGGTGGTCATAGAGTCAGGGATCTATGCCCT 960
TGGCCCAGCCCCACCCCTCCCTTATCCTGCCACTGTCAATGCTACCTTCTATCT 1020
CTTCCCTCATCTTGTGGCATGAGGAGGTGGTATGTCAGAAGAAATGGTCGA 1080
GCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTAAAAACCAAGATAACAA 1140
TCAAAATCCCAGATGCTGGCTCTATTCCCATGAAAAAGTGCATGACATATTGAGAAG 1200
ACCTACTTACAAAGTGGCATATATTGCAATTATTAAATTAAAAGATAACCTATTATAT 1260
ATTTCTTATAGAAAAAGTCTGGAAGAGTTACTTCAATTGTAGCAATGTCAGGGTGGT 1320
GGCAGTATAGGTGATTTCTTTAATTCTGTTAATTATCTGTATTCCTAATTTCT 1380
ACAATGAAGATGAATTCTGTATAAAAATAAGAAAATTAATCTTGAGGTAAGCAG 1440

FIG. 1

Figure 1

AGCAGACATCATCTCTGATTGCTCTCAGCCTCCAATTCCCCAGAGTAAATTCAAATTGAA 1500
TCGAGCTCTGCTGCTGGTTGGTAGTAGTGATCAGGAAACAGATCTCAGCAAAGCC 1560
ACTGAGGAGGAGGCTGTGCTGAGTTGTGTGGCTGGAATCTCTGGTAAGGAACCTAAAG 1620
AACAAAAATCATCTGGTAATTCTTCCTAGAAGGATCACAGCCCCCTGGGATTCCAAGGCA 1680
TTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGAATTGTGTCCCCCTCAAATTAC 1740
ATCCTCTTGGAAATCTCAGTCTGTGAGTTATTGGAGATAAGGTCTCTGCAGATGTAGT 1800
TAGTTAAGACAAGGTATGCTGGATGAAGGTAGACCTAAATTCAATATGACTGGTTCT 1860
TGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCCGGGAAGACTATGTAAAGATGA 1920
AGGCAGAGATCGGAGTTGCAGCCACAAGCTAACGAAACACCAAGGATTGTGGCAACCAT 1980
CAGAAGCTTGGAAAGAGGCAAAGAAGAATTCTTCCTAGAGGCTTAGAGGGATAACGGCT 2040
CTGCTGAAACCTTAATCTCAGACTTCCAGCCTCTGAACGAAGAAAGAATAATTCCGGC 2100
TGTGTTAACCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAAACTAACAGCTGCTA 2160
AAATGATCCCTGTCTCCTCGTGTACATTCTGTGTGTCCCCCTCCCACAATGTACCAA 2220
AGTTGTCTTGTGACCCAATAGAATATGGCAGAAGTGTGGCATGCCACTTCAAGATTA 2280
GGTTATAAAAGACACTGCAGCTACTTGAGCCCTCTCTGCCACCCACCGCCCC 2340
AATCTATCTTGGCTCACTCGCTCTGGGGAGCTAGCTGCCATGCTATGAGCAGGCCTAT 2400
AAAGAGACTTACGTGGTAAAAATGAAGTCTCCTGCCACAGCCACATTAGTGAACCTAG 2460
AAGCAGAGACTCTGTGAGATAATCGATGTTGTTAAGTTGCTCAGTTGGTCTA 2520
ACTTGTATGCAGCAATAGATAATAATGCAGAGAAAGAG (A_n) 2562

cDNA Sequence of murine IBR

GGCACGAGGGAGCCTGCTTCTACTTAGGTCTCAAATTTCCAGCCTGTCTTGCTA 60
AAATTCTCGCTTTATTCAAAATAGGGTCTACATACTGTGGAGCTCATGATGGTTCT 120
GAGTGGGCACTATGCTTCGAATGAAGGATTCAGCCTGAAGGTACTGTATGCACAA 180
TAACCAGCTGCTGGCTGGAGGACTGCACGCAGAGAAGGTCATTAAAGGTGAGGAGATCAG 240
TGTTGTCCAAATCGGGCACTGGATGCCAGTCTGTCCCCTGTCATCCTGGCGTTCAAGG 300
AGGAAGCCAGTGCCTATTTGTGGACAGAGAAAGGCCAATTCTGAAACTTGAGCCAGT 360
GAACATCATGGAGCTTACCTCGGGCCAAGGAATCAAAGAGCTTCACCTCTACCGGCG 420
GGATATGGGTCTTACCTCCAGCTCGAATCCGCTGCCTACCCAGGCTGGTCCCTGCAC 480
CTCACCGGAAGCTGACCAGCCTGTCAGGCTCACTCAGATCCCTGAGGACCCGCCTGGGA 540
TGCTCCATCACAGACTTCACTTCAGCAGTGTGACTAGGGCTGCGTGGTCCCCAAAC 600
TCCATAAGCAGAGGCAGAGTAGGCAGTGGCGGCTCCTGATAAGAGGATAGAGAGACAGAGG 660
AGCTCCACAGTAGGTGGTTACTCCTCTCCTCCCTACTGGACTCCGCTTGACCTAA 720
GGCACACAGACACTCTCTCCTGCATCCAGTGTGAAATCTCTGGTATTTGGAG 780
CTCAATGTGTAGATTCTTCAGATTGGATGGTACTACCTCTGGTGTGGAACCCAAAGAA 840
ACCACGTAGGACCAACAAAGAGCAACATAAAAGATTCTGGGTGAAGAAGAGGTGGAAC 900
TGTTCATACATAGTAAGATCTGACACAGTACCTCAGAAGTCCCTGCCATTCTTATGTTCT 960
GGAGAAAGTGGAGGGGGGTACCAAGACTTCTCTGGCTGGCTGGCCCTTCCCTCAA 1020
CCTTCTGACATCTGCAGCCTCTCATTCTGCCTTCATTCTCTGCCCTGAACCGAGA 1080
GGGTGATATCAGGATAGCTGACAGAAGATGACCAGGCACACTGTCCCTGGTTGAAACCAG 1140
AGGGGACAATAAAAACCTGATTCTGGTCTACTCACATAAAAGAAGCTGTGAACA 1200
TTAAGTGGGAAGAGATTGCTACTAAATAACATACTTGTAAATTCTATCTTAATTAAAATA 1260
TACTTCTCTATATTATATTATA(n) 1284

FIG. 2

IBR Polypeptides

(A) Human IBR polypeptide

MVLSGALCFR MKDSALKVLY LHNNQLLAGG LHAGKVIKGE EISVVPNRWL
DASLSPVILG VQGGSQCLSC GVGQEPTLTL EPVNIMELYL GAKESKSFTF
YRRDMGLTSS FESAAYPGWF LCTVPEADQP VRLTQLPENG GWNAPITDFY
FQQCD

(B) Mouse IBR polypeptide

MVLSGALCFR MKDSALKVLY LHNNQLLAGG LHAEKVIKGE EISVVPNRAL
DASLSPVILG VQGGSQCLSC GTEKGPIKL EPVNIMELYL GAKESKSFTF
YRRDMGLTSS FESAAYPGWF LCTSPEADQP VRLTQIPEDP AWDAPITDFY
FQQCD

FIG. 3

Comparison of Human and Mouse IBR Polypeptide Sequences

mIBR: 1 MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAEKVIKGEI SVVPNRALDASLSPVILG 60
MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHA KVIKGEI SVVPNR-LDASLSPVILG IBRcon.
hIBR: 1 MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEI SVVPNRWLDASLSPVILG 60

mIBR: 61 VQGGSQCLSCGTEKGPILKLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWF 120
VQGGSQCLSCG- -+P+L-LEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWF IBRcon.
hIBR: 61 VQGGSQCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWF 120

mIBR: 121 LCTSPEADQPVRLTQIPEDPAWDAPITDFYFQQCD 155
LCT-PEADQPVRLTQ+PE+-W+APITDFYFQQCD IBRcon.
hIBR: 121 LCTVPEADQPVRLTQLPENGGWNAPITDFYFQQCD 155

FIG. 4

Comparison of Human IBR and pro-IL-1ra Polypeptide Sequences

hIL-1ra: 38	FRIWDVNQKTFYLRNNQLVAGYLQGPNVNLEEKIDVV-----IEPHALFLGIHGGKM	90
	FR+ D K YL NNQL+AG L V E+I VVP + P + LG+ GG	con.
hIBR : 9	FRMKDSALKVLYLHNNQLLAGGLHAGKVIKGE	EISVVPNRWLDASLSP--VILGVQGGSQ 66
hIL-1ra: 91	CLSCVKSGDETRLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAM	150
	CLSC G E L LE VNI +L K+ K F F R D G T+SFESAA PGWFLCT	con.
hIBR : 67	CLSC-GVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVP	125
hIL-1ra: 151	EADQPVS LT NMPDEG---VMVTKFYFQE	175
	EADQPV LT +P+ G +T FYFQ+	con.
hIBR : 126	EADQPVR LT QLPENGGWNAPITDFYFQQ	153

FIG. 5

Recombinant IBR Polypeptides

MVLSGALCFR MKDSALKVLY LHNNQLLAGG LHAGKVIKGE EISVVPNRWL
DASLSPVILG VQGGSQCLSC GVGQEPTLTL EPVNIMELYL GAKESKSFTF
YRRDMGLTSS FESAAYPGWF LCTVPEADQP VRLTQLPENG GWNAPITDFY
FQQCD

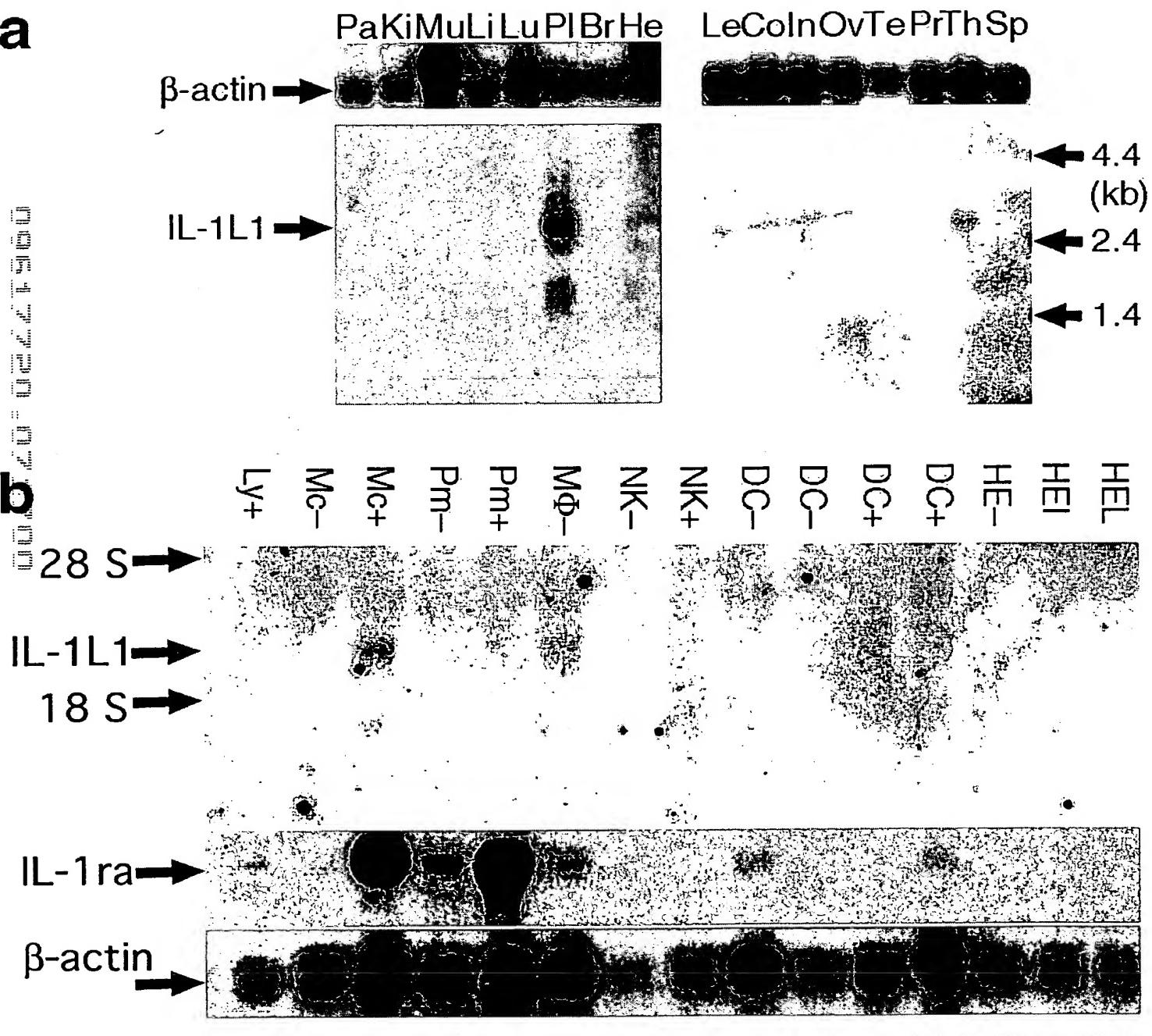
VLSGALCFR MKDSALKVLY LHNNQLLAGG LHAGKVIKGE EISVVPNRWL
DASLSPVILG VQGGSQCLSC GVGQEPTLTL EPVNIMELYL GAKESKSFTF
YRRDMGLTSS FESAAYPGWF LCTVPEADQP VRLTQLPENG GWNAPITDFY
FQQCD

GSSVLSGALCFR MKDSALKVLY LHNNQLLAGG LHAGKVIKGE EISVVPNRWL
DASLSPVILG VQGGSQCLSC GVGQEPTLTL EPVNIMELYL GAKESKSFTF
YRRDMGLTSS FESAAYPGWF LCTVPEADQP VRLTQLPENG GWNAPITDFY
FQQCD

FIG. 6

FIG. 7

a



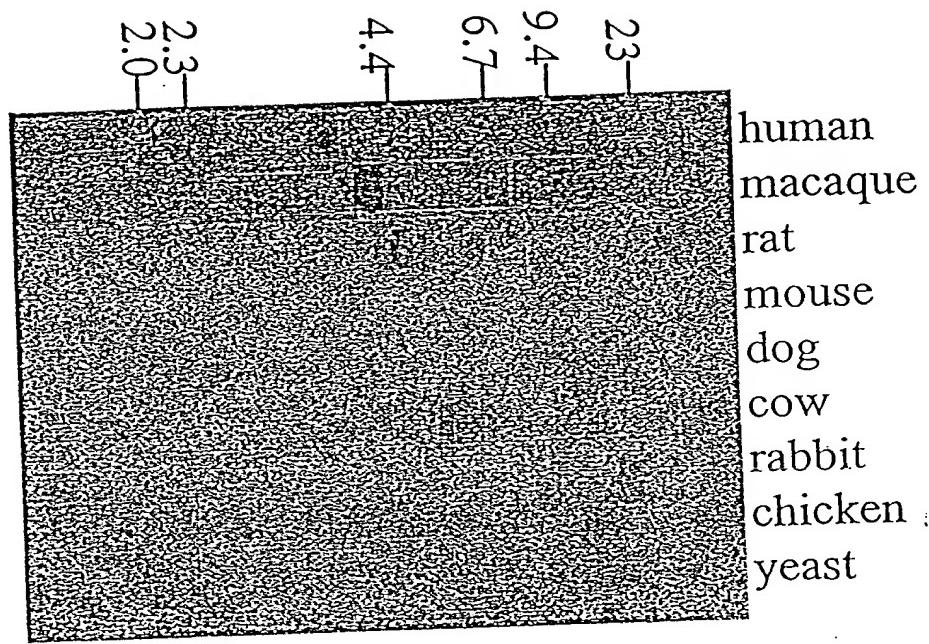


FIG. 8

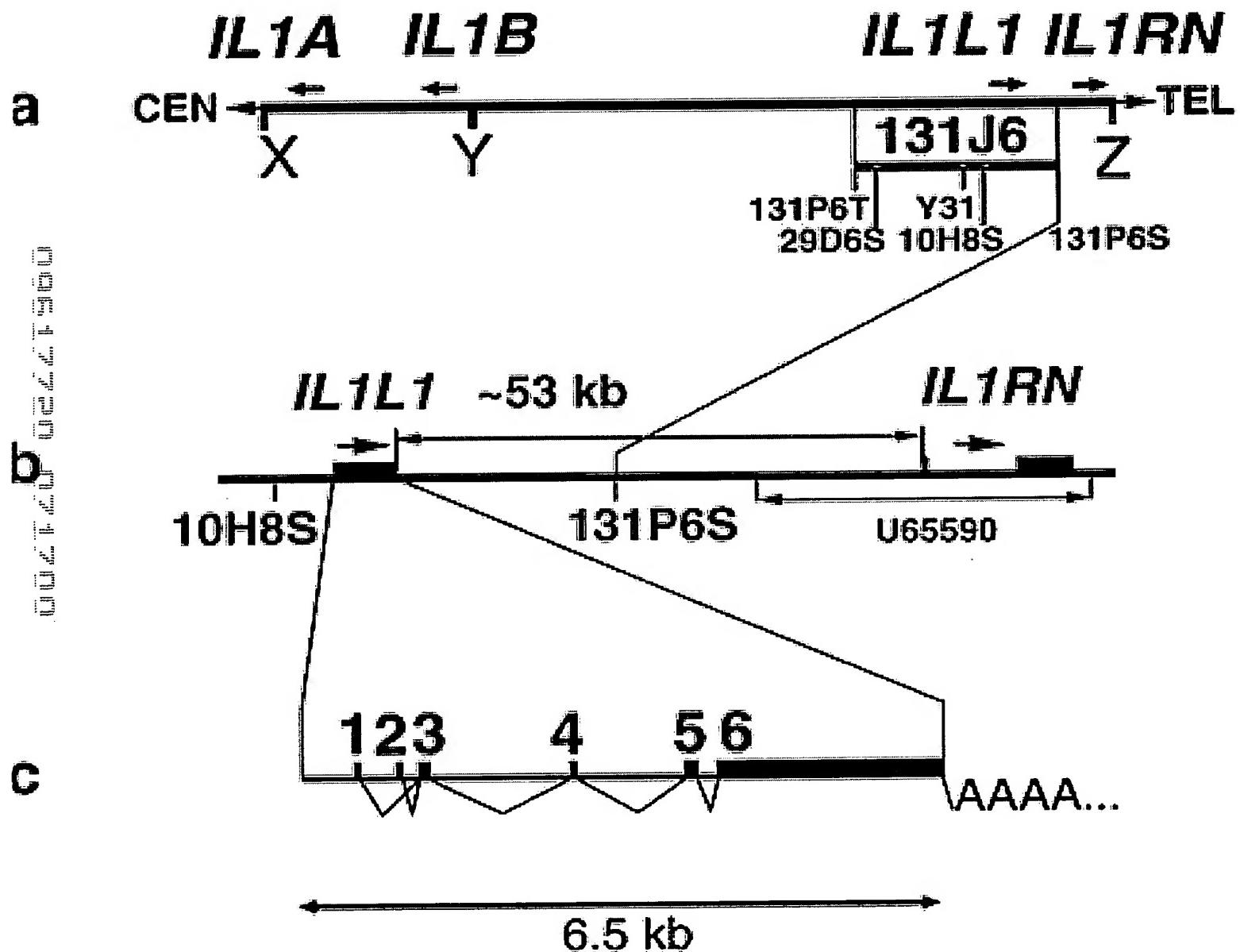


FIG. 9

a

cDNA SEQUENCES CONTAINING EXON 1
CTGGCAATGGCAGGCGAGGAAAGACAGGAAAGGAAGGGAGGGAGAAGGGAAAGGAGTGAAGGAAGGAGTGAAAAAA// exon 3

-74' M A G R K D R G R K E G E G K E *** * ***

CDNA SEQUENCES CONTAINING EXON 2
TTGGAGGAACAGGCAGACTCCACAGCTCCGCCAGGAGAAAGGAACATTCTGAG// exon 3

-54

- 54

b

5' flank	start	exon	start	seq	cdDNA	end	seq	end	3' flank
	+ 451	1	CTGGCAATGG	-74'	-	-1'	AGTGAAAAAG	+ 524	gtaaggaaaga
	+ 969	2	TTGGAGGAAC	-54	-	-1	ACATTCTGAG	+1022	gtatgctctg
tccaaaatag	+1193	3	GGGAGTCTAC	1	-	56	TGTGCTTCCG	+1248	gtgagtttat
gatgtttcag	+2631	4	AATGAAGGAC	57	-	142	GTCATTAAAG	+2716	gttgggtatg
tttcccacag	+3905	5	GTGAAGAGAT	143	-	270	AACACTAGAG	+4032	gtgagacttg
ctgccggcag	+4234	6	CCAGTGAACA	271	-	2559	AGAGAAAGAG	+6522	aaacaaatgc

C

IL-1L1 MVLSGALCFR⁽²⁾ MKDALKVLYLHNQNLLAGGLHAGKVIKG⁽¹⁾ EEISVVPNRWLDAASLSP
IL-1ra .RKSSKMQAQR⁽²⁾ IWDVNQKTFYLRNNQLVAGYLOGPNVNLEE⁽¹⁾ KIDVVP----IEPHA

IL-1L1 VILGVQGGSQCLSCG-VGQEPTLTLE⁽³⁾VNIMELYLGAKESKSFTFYRRDM...
IL-1ra LFLGIHGGKMCLSCVKGSDETRLQLE⁽³⁾VNITDLSERKQDKRFAFIRSDS...

FIG. 10

FIG. 11

1/6

1 CATGAGCAAA GATGTTAATA CAAAGATGTT TGTCACAACA TGGTTTCAA TAGCAAAAAA
61 AGAGAGAAAA ATATATAAAA GACAAATAAC AGTGGATAGG TTTCAATAAA TAATGTTACA
121 GTGATACAGT TAAATACTAT ACAGCTATTG AAGCATGTCA TTATTCAATAT TTAGTATGGA
181 AAGATATTTT GCTATTTGC TACATGAAAA AATGAGGTTG GAAAAAGTAT AGGTTTGTG
241 AATCTGTTGT ATGAAAGCTG TCTATAGTTA CATGTGTATG TGTGTGGAGG AAAAAGTGTG
301 GTCATTGGTT TTCTGATGAT GCACTCAGAA AAGACAAGTA TTCACATTTT TTCTTGTGGC
361 TGATCTGGAT TTTCAGGTTT TTCTACAATG AACATGTAGG CTGAACATTC CCTAACGAGG
421 AGAGTCCCAC CTCTAACATC TCCTGTAGGC CTGGCAATGG CAGGCAGGAA AGACAGAGGA
481 AGGAAGGAGG GAGAAGGGAA GGAGTGAAGG AAGGAGTGAA AAAGGTAAGG AAGAAAGGGA
541 ATAGGGAGG AAGGGAGGAA ATGGGAAGGG AAAGAAGGAA AGGAAGGAA GAGGGAGGGA
601 AGAAAGGAAG GGAAAAGGGA GGGAGTGAGT GAATGAAAGA TGGAAAGAAG GAAGAAAGGG
661 AGGGAGGCAG GGAGGAAAGA AAGTTGCGCT TCCCTGAGC TGCCATGGC ACTGACTCTT
721 AGGGTCTGAA AGCCCCTGAG ATGCAAAAGC CTAGTGCTCA CAAAGAGCTG GAAAGCCTCA
781 AGGAAGTTCT TCAATATTC TGGAAGGAAA CTGTCTCCAG AAGCTTCCCT CCCCACGACA
841 GATAATGAGC AGCAAGTGCT TCTGGCGACT TAGGGTGATG TGAAATCACCG CTGGGAATCC
901 TGCTCCTCCT CAGGTCTGG CAGTTTCAGG GCCCCTCCCT AGGCCTTACT TAAAAGGCTG
961 AGGCATCCTT GGAGGAACAG GCAGACTCCA CAGCTCCGC CAGGAGAAAG GAACATTCTG
1021 AGGTATGCTC TGGGGCGCTG GTGGTACCGG AGCTCTCTCC TGACCCAGA CCCAGAATCT

1081 GCTCCGTGGA GGCTGTTCAC ATGCTGGGA GCTCGGTGCA GCTGCTTGCT CCCCCAGACCC
1141 CAGCCAACTC AGCCTCTCTC TCCATGATT TCTGTTGTTT ATTCCAAAAT AGGGGAGTCT
1201 ACACCCTGTG GAGCTCAAGA TGGTCCTGAG TGGGGCGCTG TGCTTCCGGT GAGTGTATGA
1261 GGCCCTGGTT TGGTGGTGTC CTCCGGAGGA AGTGAGTTCT GGATAGACCC GTTGTCCAGC
1321 TCTGAGCAGG AGGGAGGAAG GGAGGGGCTG CCATTGCAGC TGGGAAATTG TGACCAGCAC
1381 CTCATTGCTC TTAGAGTTTT CCCAGCCTTT TTCAAATAGG GGCAGGACTG GGGCAGGCCA
1441 TCTCACAAAGG GGTCCCTGAT GCTGAGGGGG ACAAGTGAAC CTCCCAGTCT AGAGCTCCAG
1501 CCAAGTCTAT CCAAGGTGGG AACGGGGGCC AGGATCCCTG CTCAGAGCTC CGCCATTGTC
1561 CCCCCATCACA GTGAATGGAT GTAAGCTCAC CCACTCTGTG CCCCTACCTC CCTGCTACTC
1621 TTTGGGGATA ATAATAAAAC AAAAACCAT ACCATCAGCC AGTCTGTCCA CCCACTGGCA
1681 TGTACCAAGC CAGACACTCT GCCGTGTTCT GGGCTTAACA ACAGAGGATG AGAGTGGTCC
1741 TTTCTCTCAG TCTAATAAAAG CACTTCCCAC GATGTGTTCT ATGGGACTCG ATTAGAGGAG
1801 TCCCACAGAG GCATCCAGGA GATGCTTAC ACAGTGGAGC TCTCTGATCA AGTAAATGCA
1861 GGGATTCTG CTTTCTACAT CCTCTCATAA GAGAACACCA GCCCAGCTCA GCATATGAGT
1921 GACTGAGGTT TTCTGAAGTA AGGCAACTTG TTGAATCGTA TTTAGCTATG CATCGACCCA
1981 ATTTTACAC TGCATCCTT TCCCCATAT AACTTTGGA GAAACCCACT TTAGGATACA
2041 TCTTCCACCT CATAGGATGC CAGGAAATCA ACTGAGTTCA AAGATGAGAA ACAACTTTGA
2101 AAAGTTAAAT AAAAGAAATT TAAATTTAAA GAAACTCCTC ACTTAGTAAG GAATATATGA
2161 CCAAATAGAA ATACATGTAT CTTGAAGAAT TGAAGAATCA GGCTTAAACG TGGAAGAGGC

2221 CTGGATGTTA TCCAACCCAT CATCTTAGTG TAGCAATGGG GAGGCTCAGG CCCAGAGTGG
2281 GCGAGAGAGT TGTCTCCTGC GACTCAGCAG CATTGGAGGC ATAGATGGGG CAAGAACCTA
2341 GGGCTCTGAC TCACCGTGCA GCTTCTCTTC CAACAGGAGA TGGGTTGGGG CAGAAAAGGT
2401 TGAATAGGGT GAAGGGAGCAA ACCACAGACT CCAGTGGGAG ACTGTGGGGT CATCCTCCTT
2461 GTAGGGCATG AGCCCAGCAG GGCTGGGAGA CAAGGCTGTG CTGTTACTTC TGGCACAGTA
2521 GGAAGAAAGA GAGACAAAAT GCCTGAGATC AGGGGGTTCT CTGGATCCAG GGCATGCTGG
2581 AGTGTCCACC CTCCTCCTAA TGTAGTCCTC ACCCCTTCCT GATGTTTCAG AATGAAGGAC
2641 TCGGCATTGA AGGTGCTTTA TCTGCATAAT AACCAAGCTTC TAGCTGGAGG GCTGCATGCA
2701 GGGAAAGGTCA TTAAAGGTTG GTGATGAAAC ATGACCCACT TTCCTGGTC TCTATACACT
2761 CTCAGGGGAG GGGGCCTGAA GAGGGCTTAG AATAGTCATA CAGATTAGCA TAGGCCTACA
2821 GAGCCCAGGC ATTAGGGCAG CACAAACCAG GCTCTAAGCA AAGGCAAATA AAATACTACA
2881 CCTCTCAGCA AAGTGAAGAC ACACGCTCTG GGGCCACCTG AAGCTTCTGT GCAGAAGTGA
2941 GAATGTTTC CAAGAGGCTT GTCTGTCAT TCCCTTACAG GTAGATTAG GTCAAGCATT
3001 GCATTCCTG GGAGCCAGTA AGTACCAAGG AGAGAACTAA CGTAGATTCT CTATACCTTT
3061 TTTCCCATAT GGGAGTGGGT TTCTGCCTCT CCACCCCTGGG TCCCCTCTGC TCTCTGAAGA
3121 TCCTCAGTCA CTTAGAGTGG AGGGACCCAG AGAACAGGTG GCATTGTTGG ACCTCCTGCT
3181 TGCTCACTCT GCCCCATGCA CTGCAACAGG TCCCTCTCTA AAATAGTTG CACCTGCCA
3241 CCTGGGGCAC CCTTGCTGAG CACAGATGCC AGGTAGATCC TTCAGCTAGG CCATATGTGT
3301 ATGTGTGTGC TTACTGGTGT ATGTATGTGT GCATGCAGGC ATATATGTGT GAGCATATGT

3361 GTGCATGCAT GTATCTGTAT GTAACCATGT ATGTGTGAGT GCAGGTATGT AGGTATGAGC
3421 ATGTGTGTGT ATATGTATAT GTGTGCATGC ATGTATCTGT GCATGTATGT ATCTGATGTA
3481 TGTGGGTGGT GAGGGGATGT ACAGAGAGGA ATGAGACCCCT CTTTGCTCT CAGCAACCTC
3541 ACAGGGTGTA GAAAGTTGTC CAAACAATTG CAAAGGGGGG CTTATTAAGA CAGGGTTCA
3601 AAAAAGGCCT GAGACCCAAG GGGCATTAAA GGAGGGGGTT GAGTCTATTT TGGGTTGTAG
3661 AGGCTTGAAG ATTTGACCCCT GAACTAGAGG GTGGAGTGGA GGTGGTACAA TGTGCTTCCA
3721 TGCCTTGATG TCCACTCTGG GCCAGTGGAC AGGAGAAGCC ATGTCATGAC AGCTGCTGAG
3781 AAGCCTCCCT TCTGCCAGC CTGGGGCAG GCCGTCTCAC AGCAGTCCTG TGCCCTAGAG
3841 CCCAGGACAG GGGAAAGAAGG AGGGAAAGGC ATCCAGGGCC CTGCATCTGG CCTCTTCCC
3901 ACAGGTGAAG AGATCAGCGT GGTCCCCAAT CGGTGGCTGG ATGCCAGCCT GTCCCCCGTC
3961 ATCCTGGGTG TCCAGGGTGG AAGCCAGTGC CTGTCATGTG GGGTGGGGCA GGAGCCGACT
4021 CTAACACTAG AGGTGAGACT TGGGGCATCC TCACTGGGG A CTCAGCCACA GATGCTGAGC
4081 CTACTGAAGC CGGGCAGCCC ACAGCCCTGG TGCTGTGGGA CACCCTAGCA GGATTCTGTT
4141 GATGGCAGCT TTGCCTCCCT CCTAAGGATC CTGCCAGCC CTCCCTCTGC CCCTGCTTCT
4201 GCCCTCACCT GACCTCCCT CCTCTGCCGG CAGCCAGTGA ACATCATGGA GCTCTATCTT
4261 GGTGCCAAGG AATCCAAGAG CTTCACCTTC TACCGGCGGG ACATGGGGCT CACCTCCAGC
4321 TTCGAGTCGG CTGCCTACCC GGGCTGGTTC CTGTGCACGG TGCCTGAAGC CGATCAGCCT
4381 GTCAGACTCA CCCAGCTTCC CGAGAATGGT GGCTGGAATG CCCCCATCAC AGACTTCTAC
4441 TTCCAGCAGT GTGACTAGGG CAACGTGCC CCCCAGAACTC CCTGGGCAGA GCCAGCTCGG

4501 GTGAGGGGTG AGTGGAGGAG ACCCATGGCG GACAATCACT CTCTCTGCTC TCAGGACCCC

4561 CACGTCTGAC TTAGTGGGCA CCTGACCACT TTGTCTTCTG GTTCCAGTT TGGATAAATT

4621 CTGAGAGTTG GAGCTCAGTC CACGGTCCTC CCCCACGTGGA TGGTGCTACT GCTGTGGAAC

4681 CTTGTAAAAA CCATGTGGGG TAAACTGGGA ATAACATGAA AAGATTCTG TGGGGGTGGG

4741 GTGGGGGAGT GGTGGGAATC ATTCTGCTT AATGGTAAC GACAAGTGTT ACCCTGAGCC

4801 CCGCAGGCCA ACCCATCCCC AGTTGAGCCT TATAGGGTCA GTAGCTCTCC ACATGAAGTC

4861 CTGTCACTCA CCACTGTGCA GGAGAGGGAG GTGGTCATAG AGTCAGGGAT CTATGGCCCT

4921 TGGCCCAGCC CCACCCCCCTT CCCTTAATC CTGCCACTGT CATATGCTAC CTTTCCTATC

4981 TCTTCCCTCA TCATCTTGTGTT GTGGGCATGA GGAGGTGGTG ATGTCAGAAG AAATGGCTCG

5041 AGCTCAGAAG ATAAAAGATA AGTAGGGTAT GCTGATCCTC TTTAAAAAAC CCAAGATACA

5101 ATCAAAATCC CAGATGCTGG TCTCTATTCC CATGAAAAAG TGCTCATGAC ATATTGAGAA

5161 GACCTACTTA CAAAGTGGCA TATATTGCAA TTTATTTAA TTAAAAGATA CCTATTATA

5221 TATTTCTTTA TAGAAAAAAG TCTGGAAGAG TTTACTTCAA TTGTAGCAAT GTCAGGGTGG

5281 TGGCAGTATA GGTGATTTTT CTTTTAATTC TGTAAATTAA TCTGTATTTC CTAATTTTC

5341 TACAATGAAG ATGAATTCCCT TGTATAAAAA TAAGAAAAGA AATTAATCTT GAGGTAAGCA

5401 GAGCAGACAT CATCTCTGAT TGTCCCTCAGC CTCCACTTCC CCAGAGTAAA TTCAAATTGA

5461 ATCGAGCTCT GCTGCTCTGG TTGGTTGTAG TAGTGATCAG GAAACAGATC TCAGCAAAGC

5521 CACTGAGGAG GAGGCTGTGA TGAGTTGTG TGGCTGGAAT CTCTGGTAA GGAACTTAAA

5581 GAACAAAAAT CATCTGGTAA TTCTTCCTA GAAGGATCAC AGCCCCTGGG ATTCCAAGGC

5641 ATTGGATCCA GTCTCTAAGA AGGCTGCTGT ACTGGTTGAA TTGTGTCCCC CTCAAATTCA
5701 CATCCTTCTT GGAATCTCAG TCTGTGAGTT TATTTGGAGA TAAGGTCTCT GCAGATGTAG
5761 TTAGTTAAGA CAAGGTCATG CTGGATGAAG GTAGACCTAA ATTCAATATG ACTGGTTCC
5821 TTGTATGAAA AGGAGAGGAC ACAGAGACAG AGGAGACCGG GGGAAAGACTA TGTAAAGATG
5881 AAGGCAGAGA TCGGAGTTTT GCAGCCACAA GCTAAGAAC ACCAAGGATT GTGGCAACCA
5941 TCAGAACGTT GGAAGAGGCA AAGAAGAATT CTTCCCTAGA GGCTTAGAG GGATAACGGC
6001 TCTGCTGAAA CCTTAATCTC AGACTTCCAG CCTCCTGAAC GAAGAAAGAA TAAATTCGG
6061 CTGTTTTAAG CCACCAAGGA TAATTGGTTA TGGCAGCTCT AGGAAACTAA TACAGCTGCT
6121 AAAATGATCC CTGTCTCCTC GTGTTACAT TCTGTGTGTG TCCCCTCCCA CAATGTACCA
6181 AAGTTGTCTT TGTGACCAAT AGAATATGGC AGAAAGTGATG GCATGCCACT TCCAAGATTA
6241 GGTTATAAAA GACACTGCAG CTTCTACTTG AGCCCTCTCT CTCTGCCACC CACCGCCCC
6301 AATCTATCTT GGCTCACTCG CTCTGGGGGA AGCTAGCTTC CATGCTATGA GCAGGCCTAT
6361 AAAGAGACTT ATGTGGTAAA AAATGAAGTC TCCTGCCAC AGCCACATTA GTAACCTAG
6421 AAGCAGAGAC TCTGTGAGAT AATCAATGTT TGTTGTTTA AGTTGCTCAG TTTTGGTCTA
6481 ACTTGTTATG CAGCAATAGA TAAATAATAT GCAGAGAAAG AGAAACAAAT GCATTTGTTT

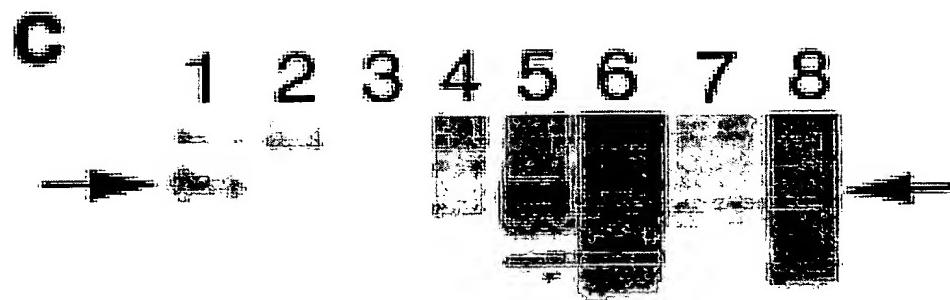
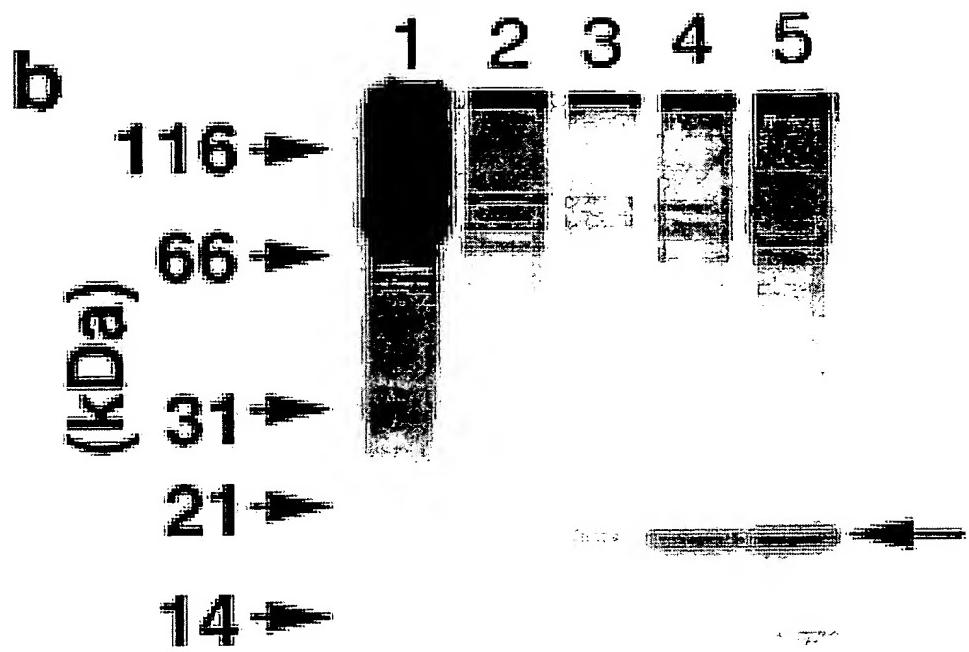
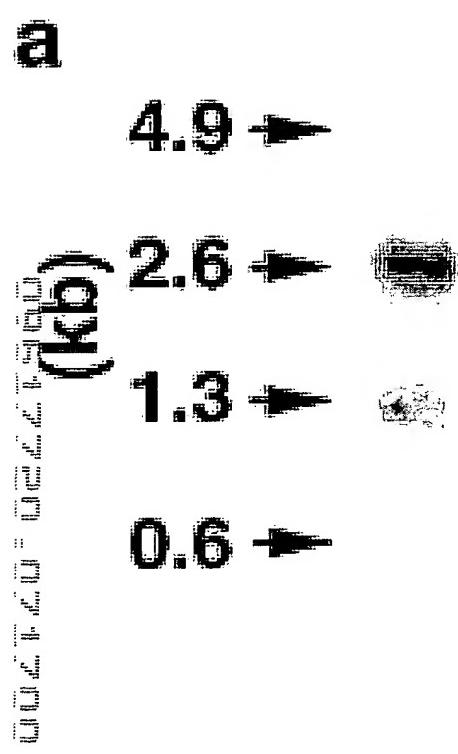


FIG. 12

	Sheet 1	Sheet 2	Sheet 3	Sheet 4
hil-111	NVLSGALCFRMKDSALKVLYLH	NNQLLAG	GLHAGKVIGKEEISVVVP	46
mrl-111	MVLSGALCFRMKDSALKVLYLH	NNQLLAG	GLHAEKVIKGEEISVVVP	46
hil-1ra	RPSGRKSSKMAFRIWDVNQKTFYLR	NNOLVAG	YLQGPNVNLEKIDWVP	50
hil-1beta	APVRSNCTLRDSQOKSLVMSGPYELKAL	HLOGQDMEQQQVFMSMF	46	
hil-1alpha	SAPFSFLSNVKYNFMRIKIYEFILNDALNQSIIRANDQYELTAALHLDEAV	KFDMGAY	59	
hil-18	YFGKLESKLSWIRNLNDQVLFIDQGNRPLIEDMTSDCDRNAP	RTIFIISMY	52	

Sheet 5 Sheet 6 Sheet 7 Sheet 8

hil-111	>>>>	>>>>	>>>>	>>>>
mrl-111	NRWLDASLSPVILGVQG	GSQCLSCG	VIGOEPTITLEPVNIMELYLGAKESKSFTFYRR	103
hil-1ra	NRALDASSISPVILGVQG	GSQCLSCG	TEKGPILKLEPVNIMELYLGAKESKSFTFYRR	103
hil-1beta	IEPHALFLGIHG	GKWCLSCVKGDETRLQLEAVNITDLSENRKODKRFAFIRS	103	
hil-1alpha	VOGEESNDKIPVALGLK	EKNLYLSCVLKDDKPTLQLESVDPKNYPK	KMEKREFENKI	104
hil-18	KSSKDAKITVILRIS	KTQIYVTAQ DEDQPVLKEMPEIPKTIT	GSETNLLEFFWE	114
	KDSQ PRGMATVCEKISTLSCE	NKISFKEMNPPDNIKDTKSDIFFEQRSVP		107

Sheet 9 Sheet 10 Sheet 11 Sheet 12

hil-111	>>>>>>	>>>>>	>>>>>	>>>>
mrl-111	DMGLITSSFESAAYPGWFCTYPEADOPVRLTOLPENGGWNAPITDFYFOQCD	155		
hil-1ra	DSGPTTSFESAACPGWFCLTAMEADOPVSLTNMPDE	152		
hil-1beta	EINNKLEFESAACPNWYISTSQAENMPVFLGGTKGGQ	153		
hil-1alpha	THGTKNYFISVAHPNLFAT KQDYWVCLAGGPP	159		
hil-18	GHDNKMOFESSSYEGVFLACEKERDLFKLIKELG	157		